

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2004, 14:48:54 ; Search time 23 Seconds  
(without alignments)  
2062.794 Million cell updates/sec

Title: US-10-063-579-70

Perfect score: 4791  
Sequence: 1 MGLFRGFVLLVCLLHQSN.....LVLSVIGSVVIVNFILSTTI 919

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/2/iaa/5A COMB.pcp.\*
  - 2: /cgn2\_6/ptodata/2/iaa/5B COMB.pcp.\*
  - 3: /cgn2\_6/ptodata/2/iaa/6A COMB.pcp.\*
  - 4: /cgn2\_6/ptodata/2/iaa/6B COMB.pcp.\*
  - 5: /cgn2\_6/ptodata/2/iaa/PTCUS COMB.pcp.\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4760	99.4	917	4	US-09-049-698-41
2	2879.5	60.1	914	4	US-09-193-562D-28
3	2879.5	60.1	914	4	US-09-623-624-6
4	2881	56.0	913	4	US-09-623-624-2
5	2431.5	50.8	903	4	US-09-193-562D-46
6	2426.5	50.6	903	4	US-09-623-624-18
7	2338.5	48.8	905	4	US-09-193-562D-2
8	2278	47.5	902	4	US-09-193-562D-34
9	2176.5	45.4	1000	4	US-09-193-562D-30
10	2103.5	43.9	795	4	US-09-193-562D-11
11	2103.5	43.9	821	4	US-09-193-562D-12
12	1950.5	40.7	943	4	US-09-643-597-161
13	1950.5	40.7	943	4	US-09-480-884A-161
14	1950.5	40.7	943	4	US-09-542-615A-161
15	1950.5	40.7	943	4	US-09-606-421B-161
16	1950.5	40.7	943	4	US-09-623-624-4
17	1950.5	40.7	943	4	US-09-221-107-161
18	1950.5	40.7	920	4	US-09-643-597-357
19	1948.5	40.7	943	4	US-09-193-562D-32
20	1913	39.9	942	4	US-09-519-172-87
21	1706	35.6	791	4	US-09-643-597-170
22	1706	35.6	791	4	US-09-480-884A-170
23	1706	35.6	791	4	US-09-542-615A-170
24	1706	35.6	791	4	US-09-606-421B-170
25	1275	26.6	592	4	US-09-643-597-169
26	1275	26.6	592	4	US-09-480-884A-169
27	1275	26.6	592	4	US-09-542-615A-169

28	1275	26.6	592	4	US-09-606-421B-169
29	987.5	20.6	342	4	US-09-193-562D-13
30	693.5	14.5	228	1	US-08-469-667-9
31	693.5	14.5	228	4	US-09-224-110-9
32	693.5	14.5	228	5	PCT-US95-07289-9
33	468	9.8	203	4	US-09-193-562D-3
34	218	4.6	40	4	US-09-049-698-45
35	174.5	3.6	1541	3	US-08-296-791-3
36	174.5	3.6	1541	4	US-09-839-996-3
37	174.5	3.6	1541	4	US-10-080-505-3
38	174.5	3.6	1541	5	PCT-US95-10661A-3
39	167	3.3	31	4	US-09-049-698-43
40	157.5	3.3	1702	3	US-08-296-791-5
41	157.5	3.3	1702	4	US-08-839-996-5
42	157.5	3.3	1702	4	US-10-080-505-5
43	157.5	3.3	1702	5	PCT-US95-10661A-5
44	151	3.2	1612	1	US-08-169-927-2
45	150	3.1	1426	3	US-09-136-574A-43

ALIGNMENTS

RESULT 1  
US-09-049-698-41  
; Sequence 41, Application US/09049698  
; Patent No. 6386732  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA A.  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: HAYDEN, MARK  
; APPLICANT: KLASS, MICHAEL R.  
; APPLICANT: ROBERTS-RAPP, LISA  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STROUPE, STEPHEN D.  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THE  
; TITLE OF INVENTION: USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
; TITLE OF INVENTION: TRACT  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,698  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/828,856  
; FILING DATE: 31-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6068.US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 917 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear																	
; MOLECULE TYPE: No. 6368792e																	
US-09-049-698-41																	
Query Match 99.4%; Score 4760; DB 4; Length 917;																	
Best Local Similarity 99.7%; Pred. No. 0;																	
Matches 916; Conservative 0; Mismatches 1; Indels 2; Gaps 1;																	
QY	1	MGLFRGFVLLVLC	11	CLHQSNTSF	1	IKLNNNG	1	PEDIV	1	VIDPSV	1	PEDEK	1	IEIOED	1	MVTTAS	60
DB	1	MGLFRGFVLLVLC	11	CLHQSNTSF	1	IKLNNNG	1	PEDIV	1	VIDPSV	1	PEDEK	1	IEIOED	1	MVTTAS	60
QY	61	TYLFEATEKRF	1	FFKXVSI	1	LIPEN	1	NKEN	1	POYKRP	1	KHENH	1	KHADVI	1	VAPPTL	120
DB	61	TYLFEATEKRF	1	FFKXVSI	1	LIPEN	1	NKEN	1	POYKRP	1	KHENH	1	KHADVI	1	VAPPTL	120
QY	121	FTECEKEGEY	1	HTFTD	1	LLGKQ	1	NEYG	1	PPGKL	1	FVHEW	1	AHLRWG	1	VDFEYNE	180
DB	121	FTECEKEGEY	1	HTFTD	1	LLGKQ	1	NEYG	1	PPGKL	1	FVHEW	1	AHLRWG	1	VDFEYNE	180
QY	181	KIEATRC	1	SAGIS	1	GRNRVY	1	KCGG	1	SLRAC	1	IDST	1	TKLYG	1	KDCOFF	240
DB	181	KIEATRC	1	SAGIS	1	GRNRVY	1	KCGG	1	SLRAC	1	IDST	1	TKLYG	1	KDCOFF	240
QY	241	QSIDS	1	VWFEC	1	NEKTH	1	QNEAPS	1	LNKCN	1	FRST	1	WEVINS	1	EDFKNT	300
DB	241	QSIDS	1	VWFEC	1	NEKTH	1	QNEAPS	1	LNKCN	1	FRST	1	WEVINS	1	EDFKNT	300
QY	301	KISQ	1	IVCLV	1	DKSG	1	MGKOR	1	LNRM	1	NOAKH	1	FLLOT	1	VENG	360
DB	301	KISQ	1	IVCLV	1	DKSG	1	MGKOR	1	LNRM	1	NOAKH	1	FLLOT	1	VENG	360
QY	361	QIKSD	1	ERNL	1	MAGL	1	PTPLG	1	TSIC	1	SGIK	1	YAFQ	1	VIGEL	420
DB	361	QIKSD	1	ERNL	1	MAGL	1	PTPLG	1	TSIC	1	SGIK	1	YAFQ	1	VIGEL	420
QY	421	SCIDEV	1	KQSGA	1	LVIH	1	FALGR	1	AADEA	1	VIEM	1	SKITG	1	SHFV	480
DB	421	SCIDEV	1	KQSGA	1	LVIH	1	FALGR	1	AADEA	1	VIEM	1	SKITG	1	SHFV	480
QY	481	TDLSQ	1	SLQES	1	KGLTL	1	NSN	1	AMND	1	TVI	1	IDST	1	VGKDT	540
DB	481	TDLSQ	1	SLQES	1	KGLTL	1	NSN	1	AMND	1	TVI	1	IDST	1	VGKDT	540
QY	541	ENFTV	1	DATSK	1	MAVLS	1	IPGTAK	1	VTW	1	AYNL	1	QAKAN	1	PETL	600
DB	541	ENFTV	1	DATSK	1	MAVLS	1	IPGTAK	1	VTW	1	AYNL	1	QAKAN	1	PETL	600
QY	601	NKD	1	VNSFP	1	PMI	1	VYAI	1	LOQ	1	YVPL	1	GANT	1	TAFTES	660
DB	601	NKD	1	VNSFP	1	PMI	1	VYAI	1	LOQ	1	YVPL	1	GANT	1	TAFTES	660
QY	661	YSRY	1	FYTA	1	YENG	1	RYSL	1	KVRAH	1	GGA	1	NTAR	1	LKRL	720
DB	661	YSRY	1	FYTA	1	YENG	1	RYSL	1	KVRAH	1	GGA	1	NTAR	1	LKRL	720
QY	721	EDTQ	1	TLE	1	DFSR	1	TAS	1	GAFV	1	VS	1	QVPS	1	LPDQ	780
DB	721	EDTQ	1	TLE	1	DFSR	1	TAS	1	GAFV	1	VS	1	QVPS	1	LPDQ	780
QY	781	FDV	1	GKQ	1	RYV	1	IRIS	1	AS	1	ILDR	1	SFDD	1	ALQV	840
DB	781	FDV	1	GKQ	1	RYV	1	IRIS	1	AS	1	ILDR	1	SFDD	1	ALQV	840
QY	841	IFIA	1	IKS	1	DKS	1	NT	1	SKV	1	SNIA	1	QVTL	1	FI	900
DB	841	IFIA	1	IKS	1	DKS	1	NT	1	SKV	1	SNIA	1	QVTL	1	FI	900
QY	901	VLS	1	VIG	1	SW	1	VN	1	FL	1	ST	1	TI	1	919	
DB	899	VLS	1	VIG	1	SW	1	VN	1	FL	1	ST	1	TI	1	917	

Query Match 60.1%; Score 2879.5; DB 4; Length 914;  
Best Local Similarity 61.6%; Pred. No. 8.3e-248;  
Matches 563; Conservative 124; Mismatches 216; Indels 11; Gaps 8;

QY 1 MGLFRGFVFLVLC 11 CLHQS-N 1 TSF 1 KLNNG 1 PEDIV 1 VIDPSV 1 PEDEK 1 IEIOED 1 MVTTAS 1 59  
DB 1 MGLFRGFVFLVLC 11 CLHQS-N 1 TSF 1 KLNNG 1 PEDIV 1 VIDPSV 1 PEDEK 1 IEIOED 1 MVTTAS 1 60  
QY 60 STYLFEATEKRF 1 FFKXVSI 1 LIPEN 1 NKEN 1 POYKRP 1 KHENH 1 KHADVI 1 VAPPTL 1 PGRDEPYTK 1 119  
DB 61 SYLFEATGR 1 FFKXVSI 1 LIPET 1 WTKT 1 KADY 1 VRPK 1 LETY 1 KNAD 1 VLVA 1 ESTPP 1 GNDPEYTE 1 120  
QY 120 OFTECEKEGEY 1 HTFTD 1 LLGKQ 1 NEYG 1 PPGKL 1 FVHEW 1 AHLRWG 1 VDFEYNE 1 DQPYRAKSK 1 179  
DB 121 QMNCCEKEGEY 1 HTFTD 1 LLGKQ 1 NEYG 1 PPGKL 1 FVHEW 1 AHLRWG 1 VDFEYNE 1 DQPYRAKSK 1 180  
QY 180 KKTAEATRC 1 SAGIS 1 GRNRVY 1 KCGG 1 SLRAC 1 IDST 1 TKLYG 1 KDCOFF 1 PPDKV 1 TEKASIMFM 1 239  
DB 181 -RQAVRCS 1 AGITG 1 TVVVK 1 KCGG 1 CVTK 1 KCTF 1 NKVT 1 GLY 1 EKG 1 CEF 1 VLOS 1 RQTEKASIMFM 1 239  
QY 240 MQSIDS 1 VWFEC 1 NEKTH 1 QNEAPS 1 LNKCN 1 FRST 1 WEVINS 1 EDFKNT 1 IPMT 1 PTPPPPPV 1 299  
DB 240 AQHVD 1 SIVEF 1 CTE 1 QNHN 1 KEAP 1 NQON 1 KNR 1 STW 1 EIR 1 DSE 1 FPK 1 TPT 1 MT 1 QPN 1 TFS 1 299  
QY 300 LKTSQ 1 RIVCLV 1 DKSG 1 MGKOR 1 LNM 1 NOAKH 1 FLLOT 1 VENG 1 SWGVH 1 FDS 1 AT 1 VNK 1 359  
DB 300 LQIGQR 1 IVCLV 1 DKSG 1 SMAT 1 GNL 1 RL 1 NQ 1 AQL 1 FLLOT 1 VENG 1 SWGVH 1 FDS 1 AAH 1 QSEL 1 359  
QY 360 IQIKSD 1 ERN 1 L 1 MAGL 1 PTPLG 1 TSIC 1 SGIK 1 YAFQ 1 VIGEL 1 HSOLD 1 SGEVL 1 L 1 TDGEDNTA 1 419  
DB 360 IQINSG 1 SDR 1 TLAK 1 RL 1 PAA 1 AS 1 GGT 1 SIC 1 SL 1 R 1 SAFT 1 V 1 R 1 K 1 Y 1 - 1 P 1 TD 1 G 1 SE 1 V 1 LL 1 TD 1 G 1 S 1 D 1 NT 1 418  
QY 420 SSCIDEV 1 KQSGA 1 LVIH 1 FALGR 1 AADEA 1 VIEM 1 SKITG 1 SHFV 1 VSDEA 1 QNGGLI 1 DAFGALTSG 1 479  
DB 419 SGC 1 FNEV 1 KQSGA 1 LVIH 1 FALGR 1 AADEA 1 VIEM 1 SKITG 1 SHFV 1 VSDEA 1 QNGGLI 1 DAFGALTSG 1 478  
QY 480 NTDLSQ 1 SLQES 1 KGLTL 1 NSN 1 AMND 1 TVI 1 IDST 1 VGKDT 1 FFLI 1 TWNSL 1 PPSIS 1 LWD 1 SGTI 1 539  
DB 479 NGAYS 1 QRS 1 IQES 1 KGLTL 1 NSN 1 AMND 1 TVI 1 IDST 1 VGKDT 1 FFLI 1 TWNSL 1 PPSIS 1 LWD 1 SGTI 1 538  
QY 540 MENT 1 TVD 1 ATSK 1 MAVLS 1 IPGTAK 1 VTW 1 AYNL 1 QAKAN 1 PETL 1 TI 1 TVTS 1 RAANS 1 SV 1 PPI 1 TVNAK 1 599  
DB 539 QGGE 1 FV 1 DK 1 TMA 1 YL 1 Q 1 PG 1 IAK 1 VGT 1 WK 1 Y 1 SI 1 Q 1 ASS 1 - 1 OT 1 L 1 T 1 TV 1 TS 1 RA 1 SN 1 AL 1 PPI 1 TVTSK 1 596  
QY 600 MNK 1 VNS 1 F 1 P 1 PM 1 I 1 V 1 Y 1 A 1 I 1 LO 1 Q 1 Y 1 V 1 PL 1 G 1 AN 1 TA 1 FTES 1 QNGH 1 TE 1 V 1 LE 1 LD 1 NG 1 AG 1 ADS 1 F 1 K 1 ND 1 G 1 659  
DB 597 TNKT 1 S 1 F 1 P 1 PL 1 V 1 Y 1 AN 1 R 1 Q 1 GAS 1 IL 1 RA 1 SV 1 TAL 1 IES 1 VNG 1 KT 1 VT 1 L 1 Q 1 LD 1 NG 1 AG 1 AD 1 T 1 K 1 DD 1 G 1 656  
QY 660 VYSRY 1 FYTA 1 YENG 1 RYSL 1 KVRAH 1 GGA 1 NTAR 1 LKRL 1 PP 1 LNRAA 1 YI 1 PGW 1 VVNG 1 IEAN 1 PPR 1 PEI 1 719  
DB 657 VYSRY 1 FYTT 1 YD 1 TN 1 GR 1 YSV 1 KV 1 RA 1 LG 1 VNA 1 RR 1 RV 1 PQ 1 QS 1 GAL 1 YI 1 PGW 1 IEAN 1 DE 1 SI 1 QN 1 MPP 1 PEI 1 716  
QY 720 D-EDT 1 QT 1 LE 1 D 1 F 1 SR 1 T 1 AS 1 G 1 AF 1 V 1 VS 1 Q 1 V 1 PS 1 L 1 P 1 D 1 Q 1 Y 1 PP 1 S 1 Q 1 IT 1 D 1 L 1 D 1 AT 1 V 1 H 1 E 1 DK 1 I 1 - 1 L 1 T 1 W 1 T 1 A 1 P 1 777

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2004, 14:43:13 ; Search time 50 Seconds  
(without alignments)  
5799.225 Million cell updates/sec

Title: US-10-063-579-70

Perfect score: 4791  
Sequence: 1 MGLFRGFVLLVLCILHQS.....LVLSVIGSVVIVNFILSTTI 919

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*  
1: sp\_archea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4763	99.4	917	Q9UNF7	Q9unf7 homo sapien
2	2884.5	60.2	914	Q3UPC6	Q3upc6 homo sapien
3	2882.5	60.2	914	Q35151	Q35151 homo sapien
4	2879.5	60.1	914	Q9UNF6	Q9unf6 homo sapien
5	2765	57.7	917	Q9TUB5	Q9tub5 sus scrofa
6	2681	56.0	913	Q9D7Z6	Q9d7z6 mus musculus
7	2677	55.9	913	Q8R049	Q8r049 mus musculus
8	2396	50.0	469	Q9NXPI	Q9nxpi homo sapien
9	2343.5	48.9	909	Q91ZF5	Q91zf5 mus musculus
10	2343	48.9	902	Q9EQR4	Q9eqr4 mus musculus
11	2341.5	48.9	905	6	O18741 bos taurus
12	2333	48.7	902	11	Q9R070 mus musculus
13	2332	48.7	902	11	Q9QX15 mus musculus
14	2331	48.7	902	11	Q8C324 mus musculus
15	2324	48.5	902	11	Q8CCM1 mus musculus
16	2319.5	48.4	901	11	O88860 mus musculus

17	2107	44.0	820	6	O18743
18	2104.5	43.9	794	6	O18742
19	1950.5	40.7	943	4	Q9Y6N2
20	1941.5	40.5	943	4	Q9UQC9
21	1882.5	39.3	942	11	Q8BZ22
22	1446	30.2	674	11	Q8BZFF
23	1326.5	27.7	513	11	O91Z28
24	1050	21.9	337	11	O8C9E1
25	987.5	20.6	342	6	O18744
26	741	15.5	262	4	Q9Y6N3
27	295	6.2	1004	17	O8PU63
28	220	4.6	109	6	O29282
29	185	3.9	494	5	O9U7P4
30	177	3.7	1154	16	Q7U5X7
31	174.5	3.6	589	17	O8TU27
32	173.5	3.6	842	16	O897H0
33	168	3.5	6310	16	O88PP2
34	163	3.4	1450	16	Q9CE07
35	161	3.4	1643	2	Q9F0P6
36	160	3.4	1386	16	Q92DL0
37	159.5	3.3	3624	16	O8Z411
38	159.5	3.3	3624	16	O83SZ3
39	159	3.3	906	17	O8TFI9
40	156.5	3.3	589	10	O8LQ58
41	156	3.3	1270	3	Q9Y743
42	155.5	3.2	3283	16	O8ZIS2
43	154	3.2	1086	5	O18428
44	153.5	3.2	650	10	O84WA3
45	153.5	3.2	676	10	Q9MIS2

## ALIGNMENTS

### RESULT 1

Q9UNF7 PRELIMINARY; PRT; 917 AA.  
 ID Q9UNF7;  
 AC Q9UNF7;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Calcium-activated chloride channel protein 2.  
 GN CAC2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RX MEDLINE=9364503; PubMed=10437792;  
 RA Agnel M., Vermat T., Culouscou J.M.;  
 RT "Identification of three novel members of the calcium-dependent  
 RT chloride channel (CaCC) family predominantly expressed in the  
 RT digestive tract and trachea.";  
 RL FEBS Lett. 455:295-301(1999).  
 DR ENBL; AF127035; AAD48398.1; --  
 DR Genew; HGNC:2018; CLCA4.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0006810; P:transport; TAS.  
 DR InterPro; IPR004727; CaCC\_prot1.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF00092; vwa; 1.  
 DR SMART; SM00327; VWA; 1.  
 DR TIGRFAMS; TIGR00868; hCaCC; 1.  
 DR PROSITE; PS50234; VWFA; 1.  
 DR PROSITE; PS50234; VWFA; 1.  
 SQ SEQUENCE 917 AA; 101153 MW; EA01090D781BEB95 CRC64;

Query Match 99.4%; Score 4763; DB 4; Length 917;  
 Best Local Similarity 99.7%; Pred. No. 2.1e-295;  
 Matches 916; Conservative 0; Mismatches 1; Indels 2; Gaps 1;  
 QY 1 MGLFRGFVLLVLCILHQSNTSFIKNNNGFEDIVIDPSVPEDEKIEQIEDMVTAS 60

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Db 1 MGLFRGFVFLVLLCLLHQSNTSPFKLNNGFEDIVVIDSPVEDEKILIEQIEDMTTAS 60
Qy 61 TYLFEATEKEKFFKFNKNSILLIPENKKNPOYKPKHENHKAHVIVAPPTLPGRDEPYTKQ 120
Db 61 TYLFEATEKEKFFKFNKNSILLIPENKKNPOYKPKHENHKAHVIVAPPTLPGRDEPYTKQ 120
Qy 121 FTCEGEGEYIHFTPDLLGLKKQNEYGPPGKLFVHEWAHLRWGVDFEYNEDEQFFYAKSK 180
Db 121 FTCEGEGEYIHFTPDLLGLKKQNEYGPPGKLFVHEWAHLRWGVDFEYNEDEQFFYAKSK 180
Qy 181 KIEATRCAGISGRNRYKCGGSLRACRIDSTTKLYGKDCQFPDKVCTEKASIMEM 240
Db 181 KIEATRCAGISGRNRYKCGGSLRACRIDSTTKLYGKDCQFPDKVCTEKASIMEM 240
Qy 241 QSDSDVVEFCNEKTHNQEAFLSNQIKCNFRSTWEVINSSEDFKNTIPMTVPPPPVFSLL 300
Db 241 QSDSDVVEFCNEKTHNQEAFLSNQIKCNFRSTWEVINSSEDFKNTIPMTVPPPPVFSLL 300
Qy 301 KISORIVCLVLDKSGSGGKDRLNRMNQAOKHFLQTVENGSGVGMVHFDSTATVKNLI 360
Db 301 KISORIVCLVLDKSGSGGKDRLNRMNQAOKHFLQTVENGSGVGMVHFDSTATVKNLI 360
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## RESULT 2

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AC Q9UPC6;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
ID Q9UPC6;
BT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Calcium-dependent chloride channel-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gruber A.D., Elble R.C., Ji H.L., Schreuer K.D., Fuller C.M.,
RA Pauli B.U.;
RT "Genomic cloning, molecular characterization, and functional analysis
RT of human CLCA1, the first human member of the family of Ca2+-activated
RT Cl- channel proteins."
RL Genomics 54:200-214(1998).
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005247; P: voltage-gated chloride channel activity; IEA.
DR GO: GO:0006821; P: chloride transport; IEA.
DR GO: GO:0015992; P: proton transport; IEA.
DR InterPro: IPR00131; ATPase gamma.
DR InterPro: IPR004727; CaCC_prot1.
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DR Pfam: PF00092; vwa; 1.
DR SMART: SM00327; vwa; 1.
DR TIGRFAMs: TIGR00868; hCaCC; 1.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gruber A.D., Elble R.C., Ji H.L., Schreuer K.D., Fuller C.M.,
RA Pauli B.U.;
RT "Genomic cloning, molecular characterization, and functional analysis
RT of human CLCA1, the first human member of the family of Ca2+-activated
RT Cl- channel proteins."
RL Genomics 54:200-214(1998).
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DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00092; vwa; 1.
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Matches 564; Conservative 124; Mismatches 215; Indels 11; Gaps 8;

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GenCore version 5.1.6  
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Run on: April 27, 2004, 04:46:55 ; Search time 158 Seconds  
(without alignments)  
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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5: /cgm2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgm2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	4760	99.4	3043	4	US-09-049-698-16	Sequence 16, Appl
2	4760	99.4	3181	4	US-09-049-698-18	Sequence 18, Appl
3	2882.5	60.2	3007	4	US-09-193-562D-27	Sequence 27, Appl
4	2879.5	60.1	2745	4	US-09-623-624-5	Sequence 5, Appl
5	2681	56.0	2931	4	US-09-623-624-1	Sequence 1, Appl
6	2341.5	48.9	3317	4	US-09-193-562D-1	Sequence 1, Appl
7	2282	47.6	3022	4	US-09-193-562D-33	Sequence 33, Appl
8	2191.5	45.7	3418	4	US-09-193-562D-29	Sequence 29, Appl
9	1950.5	40.7	2970	4	US-09-193-562D-31	Sequence 31, Appl
10	1950.5	40.7	3190	4	US-09-623-624-3	Sequence 3, Appl
11	1950.5	40.7	3951	4	US-09-643-597-160	Sequence 160, App
12	1950.5	40.7	3951	4	US-09-480-884A-160	Sequence 160, App

13	1950.5	40.7	3951	4	US-09-542-615A-160	Sequence 160, App
14	1950.5	40.7	3951	4	US-09-606-421B-160	Sequence 160, App
15	1950.5	40.7	3951	4	US-09-221-107-160	Sequence 160, App
16	1950	40.7	2773	4	US-08-643-597-358	Sequence 358, App
17	1950	40.7	8031	4	US-09-643-597-254	Sequence 254, App
18	1950	40.7	8031	4	US-09-480-884A-254	Sequence 254, App
19	1950	40.7	8031	4	US-09-542-615A-254	Sequence 254, App
20	1950	40.7	8031	4	US-09-606-421B-254	Sequence 254, App
21	1927	40.2	2784	4	US-09-643-597-168	Sequence 168, App
22	1927	40.2	2784	4	US-09-480-884A-168	Sequence 168, App
23	1927	40.2	2784	4	US-09-542-615A-168	Sequence 168, App
24	1927	40.2	2784	4	US-09-606-421B-168	Sequence 168, App
25	1913	39.9	3156	4	US-09-919-172-86	Sequence 86, Appl
26	1685	35.2	1081	4	US-09-016-434-928	Sequence 928, App
27	1685	35.2	1399	4	US-09-049-698-17	Sequence 17, Appl
28	1482	30.9	1512	4	US-09-016-434-850	Sequence 850, App
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35	875.5	18.3	576	3	US-09-385-982-23	Sequence 23, Appl
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37	736.5	15.4	611	3	US-09-385-982-27	Sequence 27, Appl
38	698	14.6	878	1	US-08-489-667-8	Sequence 8, Appl
39	698	14.6	878	4	US-09-224-110-8	Sequence 8, Appl
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43	427	8.9	242	4	US-09-049-698-8	Sequence 8, Appl
44	411	8.6	241	4	US-09-049-698-7	Sequence 7, Appl
45	408	8.5	233	4	US-09-049-698-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-09-049-698-16  
; Sequence 16, Application US/09049698  
; Patent No. 6368792  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA A.  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: HAYDEN, MARK  
; APPLICANT: KLASS, MICHAEL R.  
; APPLICANT: ROBERTS-RAPP, LISA  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STROUPE, STEPHEN D.  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THE  
; USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
; TITLE OF INVENTION: TRACT  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,698  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/829,856

FILING DATE: 31-MAR-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Becker, Cheryl L.  
 REGISTRATION NUMBER: 35,441  
 REFERENCE/DOCKET NUMBER: 6068.US.PL  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847/935-1729  
 TELEFAX: 847/938-2623  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3043 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-049-698-16

Alignment Scores:  
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 Score: 4760.00 Matches: 916  
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 Best Local Similarity: 99.67% Mismatches: 1  
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US-10-063-579-70 (1-919) x US-09-049-698-16 (1-3043)

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 Db 505 CGGTGGGAGTGTGTGATGAGTACATGAGATCAGCCCTTCTACCGTGTAAAGTCAAA 564  
 Qy 181 LysIleGluAlaThrArgCysSerAlaGlyIleSerGlyArgAsnArgValIlyLysCys 200  
 Db 565 AAAATCGAAGCAACAAGGTGTTCGACAGGTATCTCTGGTAGAAATAGAGTTTATAGGTG 624  
 Qy 201 GlnGlyGlySerCysLeuSerArgAlaCysArgIleAspSerThrThrLysLeuThrGly 220  
 Db 625 CAAGGAGGAGCTGTCTTAGTAGAGCATGACAGATTTGATCTACACAAACTGTATGGA 684  
 Qy 221 LysAspCysGlnPhePheProAspLysValGlnThrGluLysAlaSerIleMetPheMet 240  
 Db 685 AAGATTGTCAATCTCTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTATG 744  
 Qy 241 GlnSerIleAspSerValValGluPheCysAsnGluLysThrHisAsnGlnGluAlaPro 260  
 Db 745 CAAGTATTGATCTCTGTGTGTAATTTGTACCAAAAAAACCATAATCAAGAGCTCCA 804  
 Qy 261 SerLeuGlnAsnIleLysCysAsnPheArgSerThrTTPGluValIleSerAsnSerGlu 280  
 Db 805 AGCTCAAAACATAAAGTCAATTTTGAAGTACATGGAGGTGATTAGCAATCTGAG 864  
 Qy 281 AspPheLysAsnThrIleProMetValThrProProProProValPheSerLeuLeu 300  
 Db 865 GATTTTAAACACCATACCCATGGTGCACACCATCTCCACCTCTCTCTCTCTCTCTCT 924  
 Qy 301 LysIleSerGlnArgIleValCysLeuValLeuAspLysSerGlySerMetGlyGlyLys 320  
 Db 925 AAGTCAAGTCAAGAAATGTGTGCTTAGTCTTTGATAAGTCTGGAAGCATGGGGGTAAG 984  
 Qy 321 AspArgLeuAsnArgMetAsnGlnAlaLysHisPheLeuLeuGlnThrValGluAsn 340  
 Db 985 GACCGCTAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTGAAAT 1044  
 Qy 341 GlySerTrpValGlyMetValHisPheAspSerThrAlaThrIleValAsnLysLeuIle 360  
 Db 1045 GGATCTGGTGGGTGGTGTCTCTTTGATAGTACTCCCACTATTGTAAATAAGCTAATC 1104  
 Qy 361 GlnIleLysSerSerAspGluArgAsnThrLeuMetAlaGlyLeuProThrTrpProLeu 380  
 Db 1105 CAATAAAGACAGTGTATGAAGAAACACACTCATGCGAGGATACCTCATATCTCTCTG 1164  
 Qy 381 GlyGlyThrSerIleCysSerGlyIleLysTrpAlaPheGlnValIleGlyGluLeuHis 400  
 Db 1165 GGAGAACTCCATCTGCTCTGGAATTAATATGCAATTCAGTGTGATGGAGCTACAT 1224  
 Qy 401 SerGlnLeuAspGlySerGluValLeuLeuLeuThrAspGlyGluAspAsnThrAlaSer 420  
 Db 1225 TCCCACTCGATGGATCGAAGTACTGTGCTGACTGATGGGAGGATAACACTGCAAGT 1284  
 Qy 421 SerCysIleAspGluValLysGlnSerGlyAlaIleValHisPheIleAlaLeuGlyArg 440  
 Db 1285 TCTGTATGTAGTGAAGTGAACAAAGTGGGGCCATTGTTCATTTATTCCTTTGGGAGA 1344  
 Qy 441 AlaAlaAspGluAlaValIleGluMetSerLysIleThrGlyGlySerHisPheTrpVal 460  
 Db 1345 GTGTGTGATGAGCAGTATAGAGATGAGCAGAGATAACAGAGGGAAGTCATTTTATGTT 1404

Qy 461 SerAspGluAlaGlnAsnAsnGlyLeuIleAspAlaPheGlyAlaLeuThrSerGlyAsn 480  
 Db 1405 TCAGATGAAGTTCAGAACAAATGGGCTCATTCATGCTTTTGGGCTTTTACATCAGGAAAT 1464  
 Qy 481 ThrAspLeuSerGlnLysSerLeuGlnLeuGlnSerLysGlyLeuThrLeuAsnSerAsn 500  
 Db 1465 ATGATCTCTCCAGAGTCCCTTCAGCTCGAAGTAGAGGATTAACACATGATAGTAAT 1524  
 Qy 501 AlaTrpMetAsnAspThrValIleIleAspSerThrValGlyLysAspThrPhePheLeu 520  
 Db 1525 GCTGATGAACGACATCTCATATTCATAGTACAGTGGGAAGACACGCTTCCTTC 1584  
 Qy 521 IleThrTrpAsnSerLeuProProSerIleSerLeuTrpAspProSerGlyThrIleMet 540  
 Db 1585 ATCAGATGAACAGTCTGCTCCAGTATTTCTCTGGATCCCGAGTGGACATAATG 1644  
 Qy 541 GluAsnPheThrValAspAlaThrSerLysMetAlaThrLeuSerIleProGlyThrAla 560  
 Db 1645 GAAATTCACAGTGCATGCAACTTCCAAATGGCTATCTCAGTATTCAGGAATCGCA 1704  
 Qy 561 LysValGlyThrTrpAlaThrAsnLeuGlnAlaLysAlaAsnProGluThrLeuThrIle 580  
 Db 1705 AAGTGGGACATGGGCATACATCTTCAGCCAAAGGACCCAGAACATTAATTAAT 1764  
 Qy 581 ThrValThrSerArgAlaAlaAsnSerSerValProProIleThrValAsnAlaLysMet 600  
 Db 1765 ACAGTAACTTCGAGCAGCAAAATCTCTGTGCTCCCAATCACAGTGAATGCTAAATG 1824  
 Qy 601 AsnLysAspValAsnSerPheProSerProMetIleValThrAlaGluIleLeuGlnGly 620  
 Db 1825 AATAAGGACATAAACAGTTCGCCAGCCCAATGATTTAGCGAATTTCTACAGGA 1884  
 Qy 621 TyrValProValLeuGlyAlaAsnValThrAlaPheIleGluSerGlnAsnGlyHisThr 640  
 Db 1885 TAAGTACTCTTCTGGAGCAATGATGCTCTTCATTGAATCAAGAATGGACATACA 1944  
 Qy 641 GluValLeuGlnLeuLeuAspAsnGlyAlaGlyAlaAspSerPheLysAsnAspGlyVal 660  
 Db 1945 GAAGTTTGGAACTTTTGGATATGTCAGGCGCTGATTTCTTTCAAGAAATGATGGAGTC 2004  
 Qy 661 TyrSerArgTrpPheThrAlaThrGluAsnGlyArgTrpSerLeuLysValArgAla 680  
 Db 2005 TACTCCAGGTATTTTACAGCATATACAGAAATGGCAGATATAGCTTAAAGTTCGGCT 2064  
 Qy 681 HisGlyGlyAlaAsnThrAlaArgLeuLysLeuArgProProLeuAsnArgAlaIleTrp 700  
 Db 2065 CATGGAGGAGCAACACTGCCAGCTAAATTTACGGCTCCACTGAATAGAGCGCGTAC 2124  
 Qy 701 IleProGlyTrpValValAsnGlyGluIleGluAlaAsnProProArgProGluIleAsp 720  
 Db 2125 ATACAGCTGGGTAGTGTACCGGAAATTTGAAGCAACCCGCCACAGCTGAATTTGAT 2184  
 Qy 721 GluAspThrGlnThrThrLeuGluAspPheSerArgThrAlaSerGlyGlyAlaPheVal 740  
 Db 2185 GAGGATCTCAGACCACTTCAGAGGATTTTCAGCGAACAGCATCCGAGGTGCTATTGTG 2244  
 Qy 741 ValSerGlnValProSerLeuProLeuProAspGlnTrpProProSerGlnIleThrAsp 760  
 Db 2245 GTATCACAAGTCCCAAGCTTCCCTTGGCTGACCAATACCCACCAAGTCAANTTACAGAC 2304  
 Qy 761 LeuAspAlaThrValHisGluAspLysIleIleLeuThrTrpThrAlaProGlyAspAsn 780  
 Db 2305 CTTGATGCCAGTTCATGAGGATAAGATTTCTTACATGCAGACAGACACAGGAGATAAT 2364  
 Qy 781 PheAspValGlyLysValGlnArgTrpIleIleArgIleSerAlaSerIleLeuAspLeu 800  
 Db 2365 TTTGATGTGGAAAGTTCAACGTTATATCATAGATATAGTGAAGTATTCCTTGATCTA 2424  
 Qy 801 ArgAspSerPheAspAlaLeuGlnValAsnThrThrAspLeuSerProLysGluAla 820  
 Db 2425 AGAGACAGTTTGTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCCACCAAGGAGGCC 2484



QY 821 AsnSerLysGluSerPheAlaPheLysProGluAsnIleSerGluGluAsnAlaThrHis 840  
 Db 2485 AACTCCAAAGAAAGCTTTGCAATTAACACCAAAATATCTCAGAAAGAAATGCAACCCAC 2544  
 QY 841 IlePheIleAlaIleLysSerIleAspLysSerAsnLeuThrSerLysValSerAsnIle 860  
 Db 2545 ATAATTATGCCATTAAAGATATAGATAAAGCAATTTGACATCAAAAGATATCCACATT 2604  
 QY 861 AlaGlnValThrLeuPheIleProGlnAlaAsnProAspAspIleAspProThrProThr 880  
 Db 2605 GCAACAGTAACTTTGTTTATCCCTCAACCAATCTGATGATGATGATGATGATGATGAT 2658  
 QY 881 ProThrProThrProThrProAspLysSerHisAsnSerGlyValAsnIleSerThrLeu 900  
 Db 2659 CCTACTCTACTCTCTACTCTCTGATTAAGTATATCTCTGAGTATATTTCTACCGTG 2718  
 QY 901 ValLeuSerValIleGlySerValValIleValAsnPheIleLeuSerThrThile 919  
 Db 2719 GTATTGCTGTGATGGGTCTGTGTAATTTGTTAACTTTATTTAAAGTACCACCAT 2775

## RESULT 3

US-09-193-562D-27

; Sequence 27, Application US/09193562D

; Patent No. 6309857

; GENERAL INFORMATION:

; APPLICANT: Pauli, Benedicht U.

; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium

; TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules

; FILE REFERENCE: 18617.0052

; CURRENT APPLICATION NUMBER: US/09/193,562D

; CURRENT FILING DATE: 1998-11-17

; PRIOR FILING DATE: US/60/065, 922

; PRIOR FILING DATE: 1997-11-17

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 27

; LENGTH: 3007

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-193-562D-27

## Alignment Scores:

Pred. No.:	1-91e-301	Length:	3007
Score:	2882.50	Matches:	564
Percent Similarity:	75.16%	Conservative:	123
Best Local Similarity:	61.71%	Mismatches:	216
Query Match:	60.16%	Indels:	11
DB:	4	Gaps:	8

US-10-063-579-70 (1-919) x US-09-193-562D-27 (1-3007)

QY 1 MetGlyLeuPheArgGlyPheValPheLeuValLeuLeuCysLeuLeuHisGlnSer--- 19  
 Db 47 ATGGGGCCATTAAAGAGTTCTGTGTTCACTTGTGATTTCTACCTTCTAGAGGGGGCCCTG 106  
 QY 20 AsnThrSerPheIleLysLeuAsnAsnGlyPheGluAspIleValIleValIleAsp 39  
 Db 107 AGTAATTCATCTTCACCTGACCAACAAATGCTGATGAGCCATTTGCTTGCAATCGAC 166  
 QY 40 ProSerValProGluAspGluLysIleIleGluGlnIleGluAspMetValThrAla 59  
 Db 167 CCCAATGTGCCAAGAGTAAACACATCTTCAACAAATAAAGGACATGGTCAACCCAGCA 226  
 QY 60 SerThrTyrLeuPheGluAlaThrCluLysArgPhePhePheLysAsnValSerIleLeu 79  
 Db 227 TCTCTGTATCTCTTTGAAGCTACAGAAAGCGATTTTATTTCAAAATGTTGCCATTTG 286  
 QY 80 IleProGluAsnTrpLysGluAsnProGlnTyrLysArgProLysHisGluAsnHisLys 99  
 Db 287 ATTCCTGAAACATGGAACAAAGGCTGACATATGTGAGACCAACAAACITTGACCTACAA 346  
 QY 100 HisAlaAspValIleValAlaProProThrLeuProGlyArgAspGluProTyrThyls 119  
 Db 347 AATGCTGATGTTCTGGTGTCTGAGTCTACTCTCCAGGTAATGATGACCCCTACACTGAG 406

QY 120 GlnPheThrGluCysGlyGluLysGlyGluTyrIleHisPheThrProAspLeuLeuLeu 139  
 Db 407 CAGATGGGCAACTGTGGAGAGAGGGTGAAGAGTCCACCTCCTCCTGATTTCATTGCA 466  
 QY 140 GlyLysLysGlnAsnGluTyrGlyProGlyLysLeuPheValHisGluTrpAlaHis 159  
 Db 467 GGAAGAAAGTTAGCTGATATGGACCACCAAGGTAGGCATTTGTCATGAGTGGGCTCAT 526  
 QY 160 LeuArgTyrGlyValPheAspGluTyrAsnGluAspGlnProPheTyrArgAlaLysSer 179  
 Db 527 CTACGATGGGAGTATTTGACGAGTACATAATATGATGAGAAATCTTACTTATCCAATGGA 586  
 QY 180 LysLysIleGluAlaThrArgCysSerAlaGlyIleSerGlyArgAsnArgValTyrLys 199  
 Db 587 ---AGAAATACAGCAGTAAAGATTTTCAGCAGTATTTACTGTTACAAATGTAGTAAGAAG 643  
 QY 200 CysGlnGlyGlySerCysLeuSerArgAlaCysArgIleAspSerThrThrLysLeuTyr 219  
 Db 644 TGTCAAGGAGGAGCTGTTTACACCAAAAGATGCACATTCAATAAAGTTACAGGACTCTAT 703  
 QY 220 GlyLysAspCysGlnPhePheProAspLysValGlnThrGluLysAlaSerIleMetPhe 239  
 Db 704 GAAAGAGGATGTGAGTTGTTTCTCCAAATCCCGCCACGACGAGAGAGGCTTCTATATGTT 763  
 QY 240 MetGlnSerIleAspSerValValGluPheCysAsnGluLysThrHisAsnGlnGluAla 259  
 Db 764 GCACACATGTTGATTTCTATAGTTGAATCTGTACAGACAAACCAACCAACAAAGAGCT 823  
 QY 260 ProSerLeuGlnAsnIleLysCysAsnPheArgSerThrTrpGluValIleSerAsnSer 279  
 Db 824 CCAAAACAGCAAAATCAAAATGCAATCTCCGAGACACATGGGAAGTGCCTGATTTCT 883  
 QY 280 GluAspPheLysAsnThrIleProMetValThrProProProProValPheSerLeu 299  
 Db 884 GAGGACTTTAGAAACCACTCCTATGACACACAGCCCAAAATCCCACTTCTCATG 943  
 QY 300 LeuLysIleSerGlnArgIleValCysLeuValLeuAspLysSerGlySerMetGlyGly 319  
 Db 944 CTGCAGATTGGACAAAGAAATGTTGTTTGTAGTCTTGACAAATCTGGAAGCATGCGACT 1003  
 QY 320 LysAspArgLeuAsnArgMetAsnGlnAlaLysHisPheLeuLeuGlnThrValGlu 339  
 Db 1004 GGTAAACCGCCTCAATCGACTGAATCAACGACGCCAGCTTTTCTCTGCTCAGACAGTTGAG 1063  
 QY 340 AsnGlySerTrpValGlyMetValHisPheAspSerThrAlaThrIleValAsnLysLeu 359  
 Db 1064 CTGGGCTCTGGGTTGGATGTTGACATTTGACAGTGTGCTGCCCATGTACAAAGTGAATC 1123  
 QY 360 IleGlnIleLysSerSerAspGluArgAsnThrLeuMetAlaGlyLeuProThrTyrPro 379  
 Db 1124 ATACAGATAAACAGTGGCAGTGACAGGGACACACTCGCCCAAAAGATTACCTGCGAGCT 1183  
 QY 380 LeuGlyGlyThrSerIleCysSerGlyIleLysTyrAlaPheGlnValIleGlyGluLeu 399  
 Db 1184 TCAGAGGAGACCTCCATTTGACGGGGCTTGCATCGGCATTTACTGTGATTAGAGAAA 1243  
 QY 400 HisSerGlnLeuAspGlySerGluValLeuLeuLeuThrAspGlyGluAspAsnThrAla 419  
 Db 1244 TAT---CCAACTGATGATCTGAATTTGCTGCTGCTGACGAGTGGGAAGACACACTATA 1300  
 QY 420 SerSerCysIleAspGluValIleGlnSerGlyAlaIleValHisPheIleAlaLeuGly 439  
 Db 1301 AGTGGGTGTTTAAAGAGGTCAACAAAGTGGTGCATCTCCACACACAGCTGCGTTGGGG 1360  
 QY 440 ArgAlaAlaAspGluAlaValIleGluMetSerLysIleThrGlyGlySerHisPheTyr 459  
 Db 1361 CCTCTCTGAGCTCAAGAACTAGAGGAGCTGTCCAAATATGACAGAGGTTTACAGACATAT 1420  
 QY 460 ValSerAspGluAlaGlnAsnAsnGlyLeuIleAspAlaPheGlyAlaLeuThrSerGly 479  
 Db 1421 GCTTCAGATCAAGTTTCAGAAACAATGCCTCATTTGTTGTTGGGCCCTTTCTACAGGA 1480